

CRF Errors Corrected by the STIC Sys ms Branch

Serial Number: 09/995,804A

CRF Processing Dat : 4/3/02 # 6
 Edited by: DC
 Verified by: DC (STIC staff)

- ☐ Changed a file from non-ASCII to ASCII
- ☒ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: ENTERED
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☐ Other: _____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95



OIPE

RAW SEQUENCE LISTING DATE: 04/03/2002
 PATENT APPLICATION: US/09/995,804A TIME: 11:40:52

Input Set : A:\PTO.DC.txt
 Output Set: N:\CRF3\04032002\I995804A.raw

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:
 6 (i) APPLICANT: Engler, Jeffrey A
 7 Lee, Jae Hwy
 8 Collawan, James F
 9 Moore, Bryan A
 11 (ii) TITLE OF INVENTION: Receptor-Mediated Uptake of Peptides
 12 that Bind the Human Transferrin Receptor
 14 (iii) NUMBER OF SEQUENCES: 13
 16 (iv) CORRESPONDENCE ADDRESS:
 17 (A) ADDRESSEE: Hendricks and Assoc.
 18 (B) STREET: P.O. Box 2509
 19 (C) CITY: Fairfax
 20 (D) STATE: VA
 21 (E) COUNTRY: U.S.A
 22 (F) ZIP: 22031
 24 (v) COMPUTER READABLE FORM:
 25 (A) MEDIUM TYPE: Floppy disk
 26 (B) COMPUTER: IBM PC compatible
 27 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 28 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
 30 (vi) CURRENT APPLICATION DATA:
 C--> 31 (A) APPLICATION NUMBER: US/09/995,804A
 C--> 32 (B) FILING DATE: 29-Nov-2001
 33 (C) CLASSIFICATION:
 35 (viii) ATTORNEY/AGENT INFORMATION:
 36 (A) NAME: Hendricks, Glenna M
 37 (B) REGISTRATION NUMBER: 32,535
 38 (C) REFERENCE/DOCKET NUMBER: engler1
 40 (ix) TELECOMMUNICATION INFORMATION:
 41 (A) TELEPHONE: 703/425-8405
 42 (B) TELEFAX: 703/425-8406
 45 (2) INFORMATION FOR SEQ ID NO: 1:
 47 (i) SEQUENCE CHARACTERISTICS:
 48 (A) LENGTH: 7 amino acids
 49 (B) TYPE: amino acid
 50 (C) STRANDEDNESS: single
 51 (D) TOPOLOGY: unknown
 53 (ii) MOLECULE TYPE: peptide
 55 (iii) HYPOTHETICAL: NO
 57 (iv) ANTI-SENSE: NO
 61 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 63 His Ala Ile Tyr Pro Arg His

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64      1          5
66 (2) INFORMATION FOR SEQ ID NO: 2:
68      (i) SEQUENCE CHARACTERISTICS:
69          (A) LENGTH: 12 amino acids
70          (B) TYPE: amino acid
71          (C) STRANDEDNESS: single
72          (D) TOPOLOGY: unknown
74      (ii) MOLECULE TYPE: peptide
76      (iii) HYPOTHETICAL: NO
78      (iv) ANTI-SENSE: NO
82      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
84      Thr His Arg Pro Pro Met Trp Ser Pro Val Trp Pro
85      1          5          10
87 (2) INFORMATION FOR SEQ ID NO: 3:
89      (i) SEQUENCE CHARACTERISTICS:
90          (A) LENGTH: 7 amino acids
91          (B) TYPE: amino acid
92          (C) STRANDEDNESS: single
93          (D) TOPOLOGY: unknown
95      (ii) MOLECULE TYPE: peptide
97      (iii) HYPOTHETICAL: NO
99      (iv) ANTI-SENSE: NO
103     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
105     Ile Arg His Pro His Tyr Ala
106     1          5
108 (2) INFORMATION FOR SEQ ID NO: 4:
110     (i) SEQUENCE CHARACTERISTICS:
111         (A) LENGTH: 12 amino acids
112         (B) TYPE: amino acid
113         (C) STRANDEDNESS: single
114         (D) TOPOLOGY: unknown
116     (ii) MOLECULE TYPE: peptide
118     (iii) HYPOTHETICAL: NO
120     (iv) ANTI-SENSE: NO
124     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
126     Pro Trp Arg Pro Ser His Pro Val Trp Met Pro Thr
127     1          5          10
129 (2) INFORMATION FOR SEQ ID NO: 5:
131     (i) SEQUENCE CHARACTERISTICS:
132         (A) LENGTH: 18 base pairs
133         (B) TYPE: nucleic acid
134         (C) STRANDEDNESS: single
135         (D) TOPOLOGY: unknown
137     (ii) MOLECULE TYPE: DNA (genomic)
139     (iii) HYPOTHETICAL: NO
141     (iv) ANTI-SENSE: NO
145     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
147     TGGGATTTTG CTAAAAAC
149 (2) INFORMATION FOR SEQ ID NO: 6:

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RAW SEQUENCE LISTING

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Input Set : A:\PTO.DC.txt

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151      (i) SEQUENCE CHARACTERISTICS:
152          (A) LENGTH: 22 base pairs
153          (B) TYPE: nucleic acid
154          (C) STRANDEDNESS: single
155          (D) TOPOLOGY: unknown
157      (ii) MOLECULE TYPE: DNA (genomic)
159      (iii) HYPOTHETICAL: NO
161      (iv) ANTI-SENSE: NO
165      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
167 GTATGGGATT TTGCTAAACA AC                22
169 (2) INFORMATION FOR SEQ ID NO: 7:
171      (i) SEQUENCE CHARACTERISTICS:
172          (A) LENGTH: 28 base pairs
173          (B) TYPE: nucleic acid
174          (C) STRANDEDNESS: single
175          (D) TOPOLOGY: unknown
177      (ii) MOLECULE TYPE: DNA (genomic)
179      (iii) HYPOTHETICAL: NO
181      (iv) ANTI-SENSE: NO
185      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
187 TCTAGATCTG ATGAGTAAAG GAGAAGAA          28
189 (2) INFORMATION FOR SEQ ID NO: 8:
191      (i) SEQUENCE CHARACTERISTICS:
192          (A) LENGTH: 54 base pairs
193          (B) TYPE: nucleic acid
194          (C) STRANDEDNESS: single
195          (D) TOPOLOGY: unknown
197      (ii) MOLECULE TYPE: DNA (genomic)
199      (iii) HYPOTHETICAL: NO
201      (iv) ANTI-SENSE: NO
205      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
207 TTAAAGCTTT TAATGGCGCG GATAGATCGC ATGTTTGTAG AGCTCATCCA TGCC    54
209 (2) INFORMATION FOR SEQ ID NO: 9:
211      (i) SEQUENCE CHARACTERISTICS:
212          (A) LENGTH: 68 base pairs
213          (B) TYPE: nucleic acid
214          (C) STRANDEDNESS: single
215          (D) TOPOLOGY: unknown
217      (ii) MOLECULE TYPE: DNA (genomic)
219      (iii) HYPOTHETICAL: NO
221      (iv) ANTI-SENSE: NO
225      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
227 TAAAGCTTTT ACGGCCACAC CGGGCTCCAC ATCGGCGGGC GGTGGGTTTT GTAGAGCTCA 60
229 TCCATGCC                                68
231 (2) INFORMATION FOR SEQ ID NO: 10:
233      (i) SEQUENCE CHARACTERISTICS:
234          (A) LENGTH: 29 base pairs
235          (B) TYPE: nucleic acid
236          (C) STRANDEDNESS: single

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237         (D) TOPOLOGY: unknown
239     (ii) MOLECULE TYPE: DNA (genomic)
241     (iii) HYPOTHETICAL: NO
243     (iv) ANTI-SENSE: NO
247     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
249 GATCCCATGC GATCTATCCG CGCCATTAA                29
251 (2) INFORMATION FOR SEQ ID NO: 11:
253     (i) SEQUENCE CHARACTERISTICS:
254         (A) LENGTH: 29 base pairs
255         (B) TYPE: nucleic acid
256         (C) STRANDEDNESS: single
257         (D) TOPOLOGY: unknown
259     (ii) MOLECULE TYPE: DNA (genomic)
261     (iii) HYPOTHETICAL: NO
263     (iv) ANTI-SENSE: YES
267     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
269 GATCTTAATG GCGCGGATAG ATCGCATGG                29
271 (2) INFORMATION FOR SEQ ID NO: 12:
273     (i) SEQUENCE CHARACTERISTICS:
274         (A) LENGTH: 44 base pairs
275         (B) TYPE: nucleic acid
276         (C) STRANDEDNESS: single
277         (D) TOPOLOGY: unknown
279     (ii) MOLECULE TYPE: DNA (genomic)
281     (iii) HYPOTHETICAL: NO
283     (iv) ANTI-SENSE: NO
287     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:
289 GATCCACCCA CCGCCGCGCG ATGTGGAGCC CGGTGTGGCC GTAA    44
291 (2) INFORMATION FOR SEQ ID NO: 13:
293     (i) SEQUENCE CHARACTERISTICS:
294         (A) LENGTH: 44 base pairs
295         (B) TYPE: nucleic acid
296         (C) STRANDEDNESS: single
297         (D) TOPOLOGY: unknown
299     (ii) MOLECULE TYPE: DNA (genomic)
301     (iii) HYPOTHETICAL: NO
303     (iv) ANTI-SENSE: YES
307     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:
309 GATCTTACGG CCACACGGG CTCCACATCG GCGGGCGGTG GGTG    44

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VERIFICATION SUMMARY

DATE: 04/03/2002

PATENT APPLICATION: US/09/995,804A

TIME: 11:40:53

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L:31 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:32 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]